

FIG. 1A

GAATTCTCTGGACTGAGGCTCCAGTTCTGGCCTTTGGGG

TTCAAGATCACTGGGACCAGGCCGTGATCTCTATGCCCCGAGTCTCAACCCTCAACTGTC

ACCCCAAGGCACTTGGGACGTCTGGACAGACCGAGTCCCGGGAAGCCCCAGCACTGCC

GCTGCCACACTGCCCTGAGCCCAAATGGGGGAGTGAGAGGCCA TAG CTG TCT GGC

S1		S5		S10		S15
Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu						
ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCA CTG GTG CTC						
216		225		234		243

	S20		S25		S29	1
Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu						
CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG						
261	270		279		288	297

	5		10		15
Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro					
GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT CCC					
306	315		324		333

	20		25		30
Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr					
CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC					
351	360		369		378

	35		40		45
Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro					
AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG					
396	405		414		423

	50		55		60
Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr					
GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC					
441	450		459		468

	65		70		75
Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys					
GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC					
486	495		504		513

	80		85		90
Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp					
CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC					
531	540		549		558

100040-62456860

FIG. 1B

Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	Arg	His	Tyr
CGG	GAC	ACC	GTG	TGT	GGC	TGC	AGG	AAG	AAC	CAG	TAC	CGG	CAT	TAT
576			585			594			603			612		
Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys	Ser	Leu	Cys	Leu
TGG	AGT	GAA	AAC	CTT	TTC	CAG	TGC	TTC	AAT	TGC	AGC	CTC	TGC	CTC
621			630			639			648			657		
Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln	Asn	Thr	Val
AAT	GGG	ACC	GTG	CAC	CTC	TCC	TGC	CAG	GAG	AAA	CAG	AAC	ACC	GTG
666			675			684			693			702		
Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn	Glu	Cys	Val
TGC	ACC	TGC	CAT	GCA	GGT	TTC	TTT	CTA	AGA	GAA	AAC	GAG	TGT	GTC
711			720			729			738			747		
Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr	Lys	Leu	Cys
TCC	TGT	AGT	AAC	TGT	AAG	AAA	AGC	CTG	GAG	TGC	ACG	AAG	TTG	TGC
756			765			774			783			792		
Leu	Pro	Gln	Ile	Glu	Asn	Val	Lys	Gly	Thr	Glu	Asp	Ser	Gly	Thr
CTA	CCC	CAG	ATT	GAG	AAT	GTT	AAG	GGC	ACT	GAG	GAC	TCA	GGC	ACC
801			810			819			828			837		
Thr	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Phe	Gly	Leu	Cys	Leu	Leu
ACA	GTG	CTG	TTG	CCC	CTG	GTC	ATT	TTC	TTT	GGT	CTT	TGC	CTT	TTA
846			855			864			873			882		
Ser	Leu	Leu	Phe	Ile	Gly	Leu	Met	Tyr	Arg	Tyr	Gln	Arg	Trp	Lys
TCC	CTC	CTC	TTC	ATT	GGT	TTA	ATG	TAT	CGC	TAC	CAA	CGG	TGG	AAG
891			900			909			918			927		
Ser	Lys	Leu	Tyr	Ser	Ile	Val	Cys	Gly	Lys	Ser	Thr	Pro	Glu	Lys
TCC	AAG	CTC	TAC	TCC	ATT	GTT	TGT	GGG	AAA	TCG	ACA	CCT	GAA	AAA
936			945			954			963			972		
Glu	Gly	Glu	Leu	Glu	Gly	Thr	Thr	Thr	Lys	Pro	Leu	Ala	Pro	Asn
GAG	GGG	GAG	CTT	GAA	GGA	ACT	ACT	ACT	AAG	CCC	CTG	GCC	CCA	AAC
981			990			999			1008			1017		

FIG. 1B

[illegible]

Pro CCA	Ser AGC	Phe TTC	245 Ser AGT	Pro CCC	Thr ACT	Pro CCA	Gly GGC	250 Phe TTC	Thr ACC	Pro CCC	Thr ACC	Leu CTG	255 Gly GGC	Phe TTC
1026			1035			1044			1053			1062		
Ser AGT	Pro CCC	Val GTG	260 Pro CCC	Ser AGT	Ser TCC	Thr ACC	Phe TTC	265 Thr ACC	Ser TCC	Ser AGC	Ser TCC	Thr ACC	270 Tyr TAT	Thr ACC
1071			1080			1089			1098				1107	
Pro CCC	Gly GGT	Asp GAC	275 Cys TGT	Pro CCC	Asn AAC	Phe TTT	Ala GCG	280 Ala GCT	Pro CCC	Arg CGC	Arg AGA	Glu GAG	285 Val GTG	Ala GCA
1116			1125			1134			1143			1152		
Pro CCA	Pro CCC	Tyr TAT	290 Gln CAG	Gly GGG	Ala GCT	Asp GAC	Pro CCC	295 Ile ATC	Leu CTT	Ala GCG	Thr ACA	Ala GCC	300 Leu CTC	Ala GCC
1161			1170			1179			1188			1197		
Ser TCC	Asp GAC	Pro CCC	305 Ile ATC	Pro CCC	Asn AAC	Pro CCC	Leu CTT	310 Gln CAG	Lys AAG	Trp TGG	Glu GAG	Asp GAC	315 Ser AGC	Ala GCC
1206			1215			1224			1233			1242		
His CAC	Lys AAG	Pro CCA	320 Gln CAG	Ser AGC	Leu CTA	Asp GAC	Thr ACT	325 Asp GAT	Asp GAC	Pro CCC	Ala GCG	Thr ACG	330 Leu CTG	Tyr TAC
1251			1260			1269			1278			1287		
Ala GCC	Val GTG	Val GTG	335 Glu GAG	Asn AAC	Val GTG	Pro CCC	Pro CCG	340 Leu TTG	Arg CGC	Trp TGG	AA	<u>GGAATTC</u>		
1296			1305			1314			1323			1332		

FIG. 2

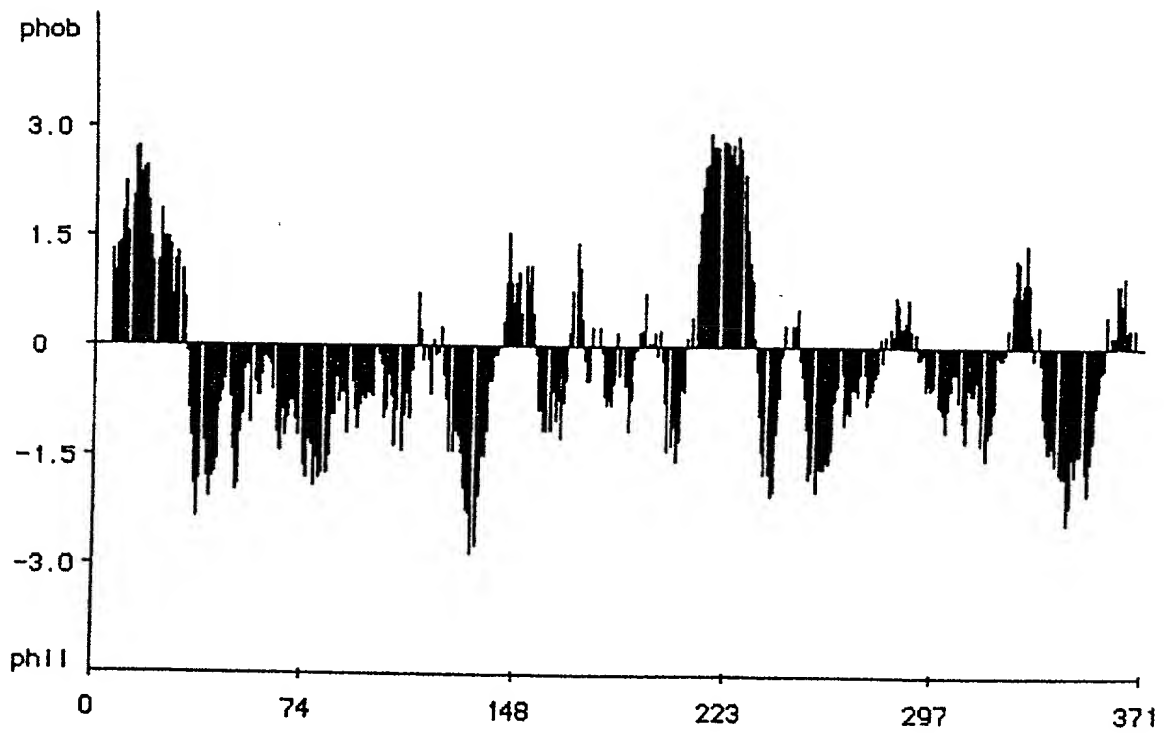
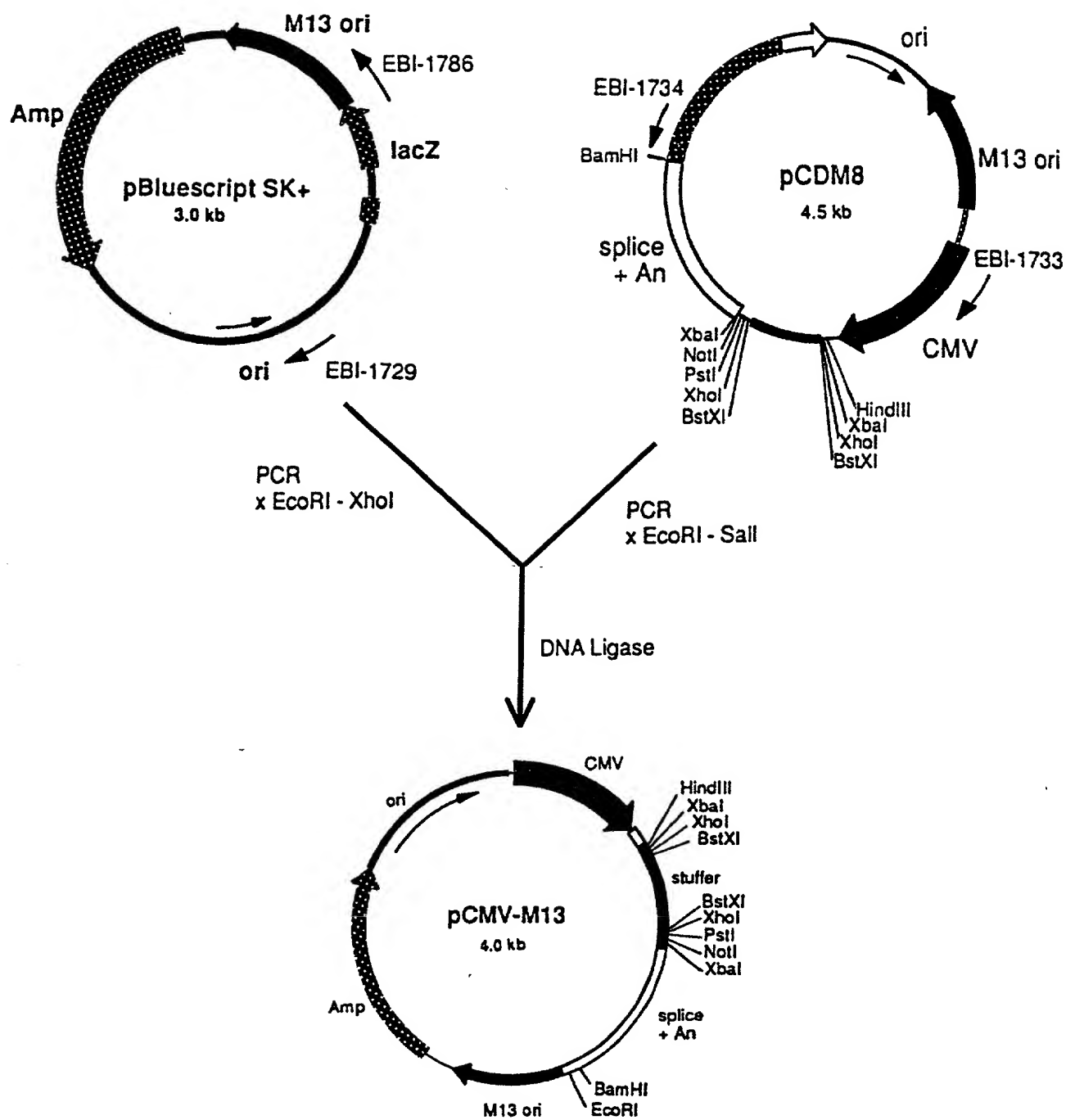
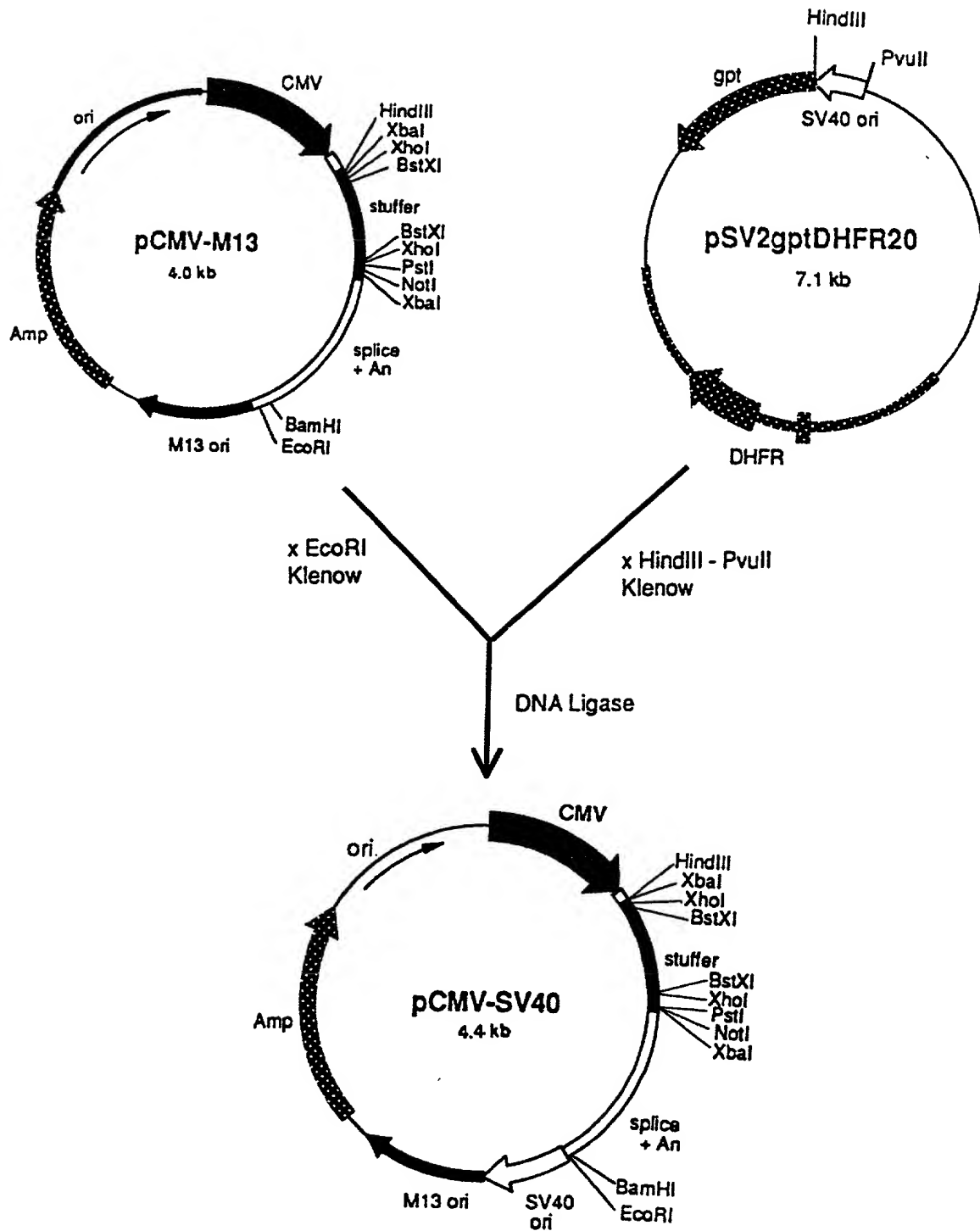


FIG. 3A



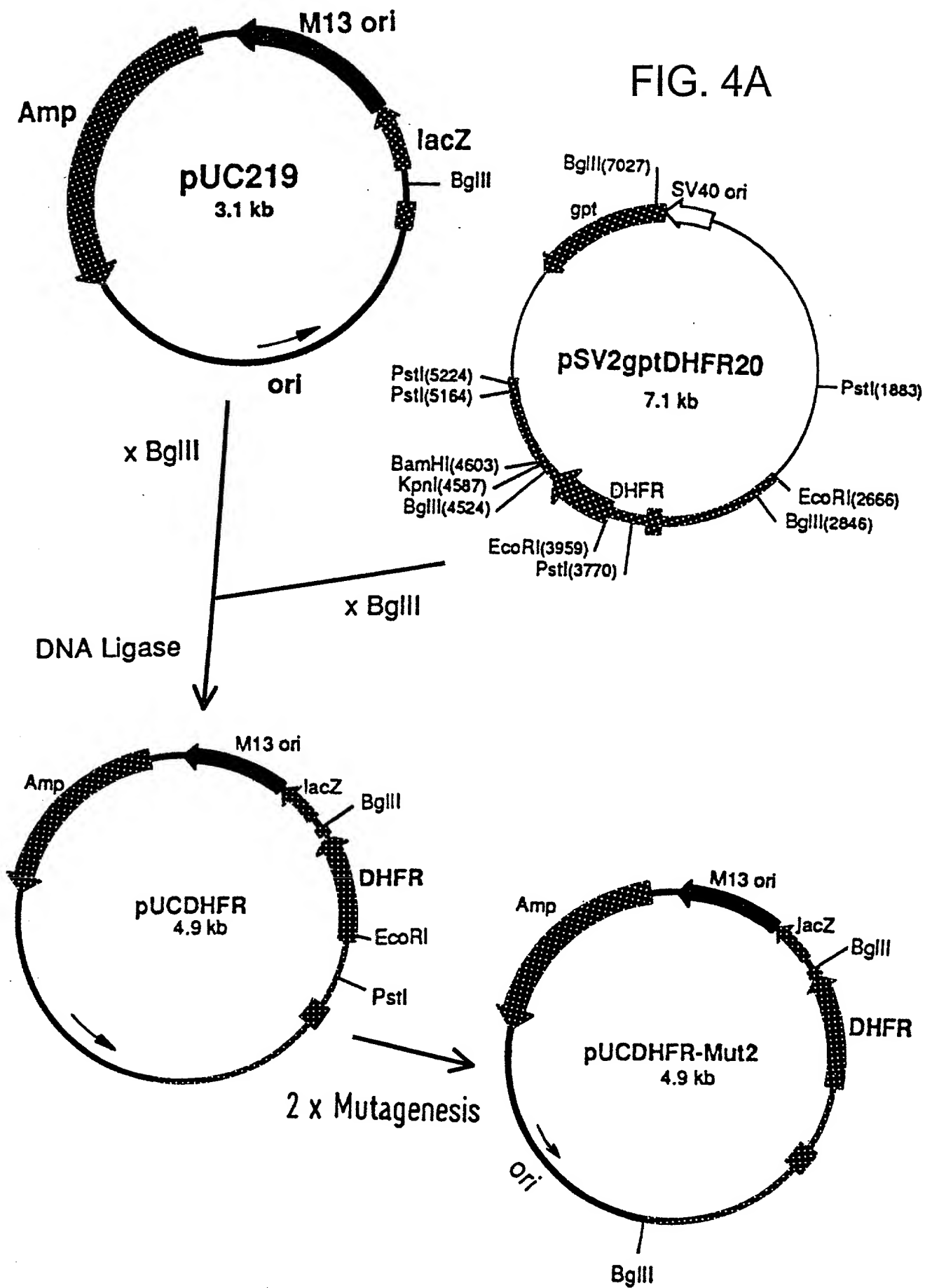
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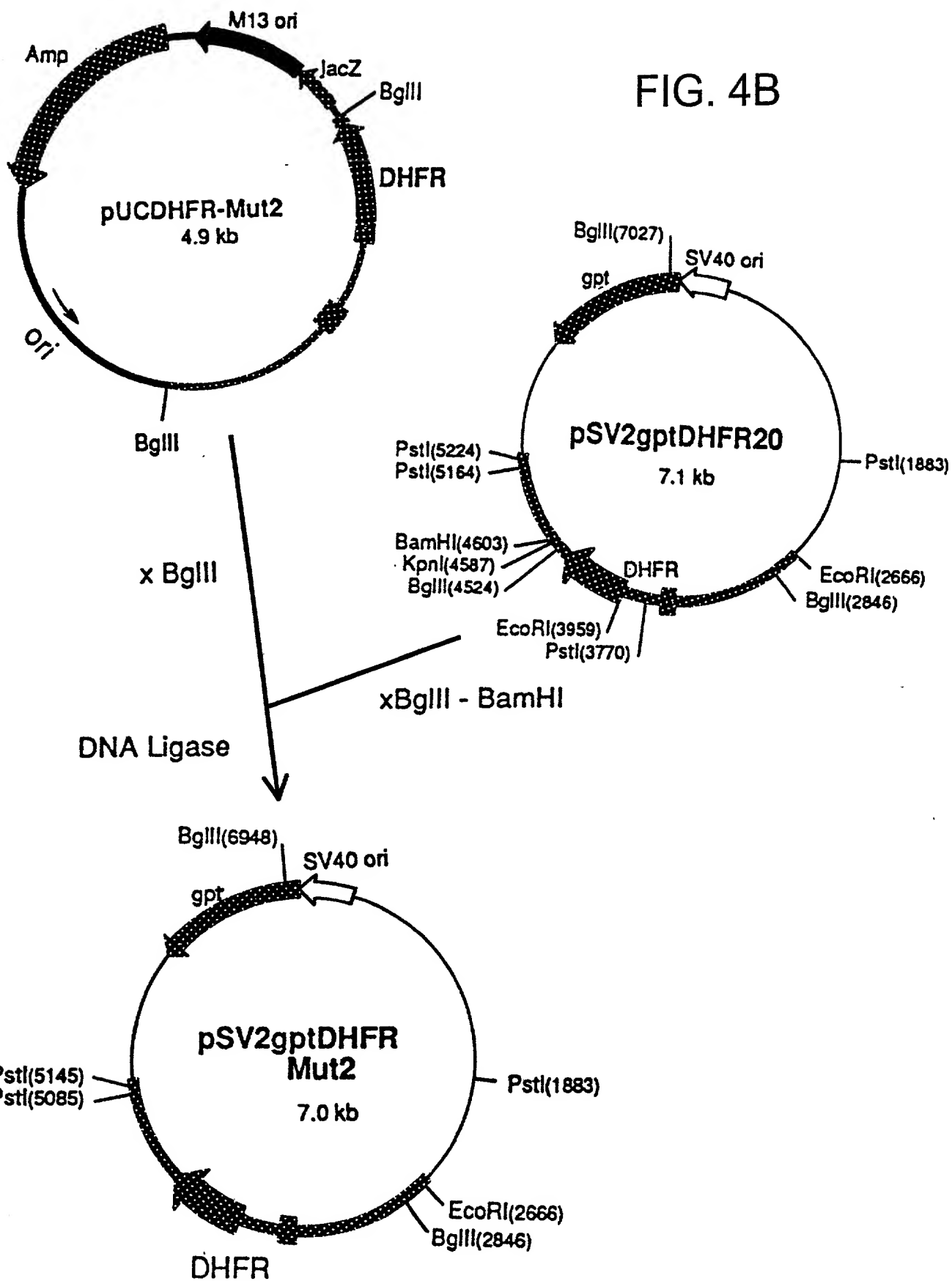
FIG. 3B



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FIG. 4A





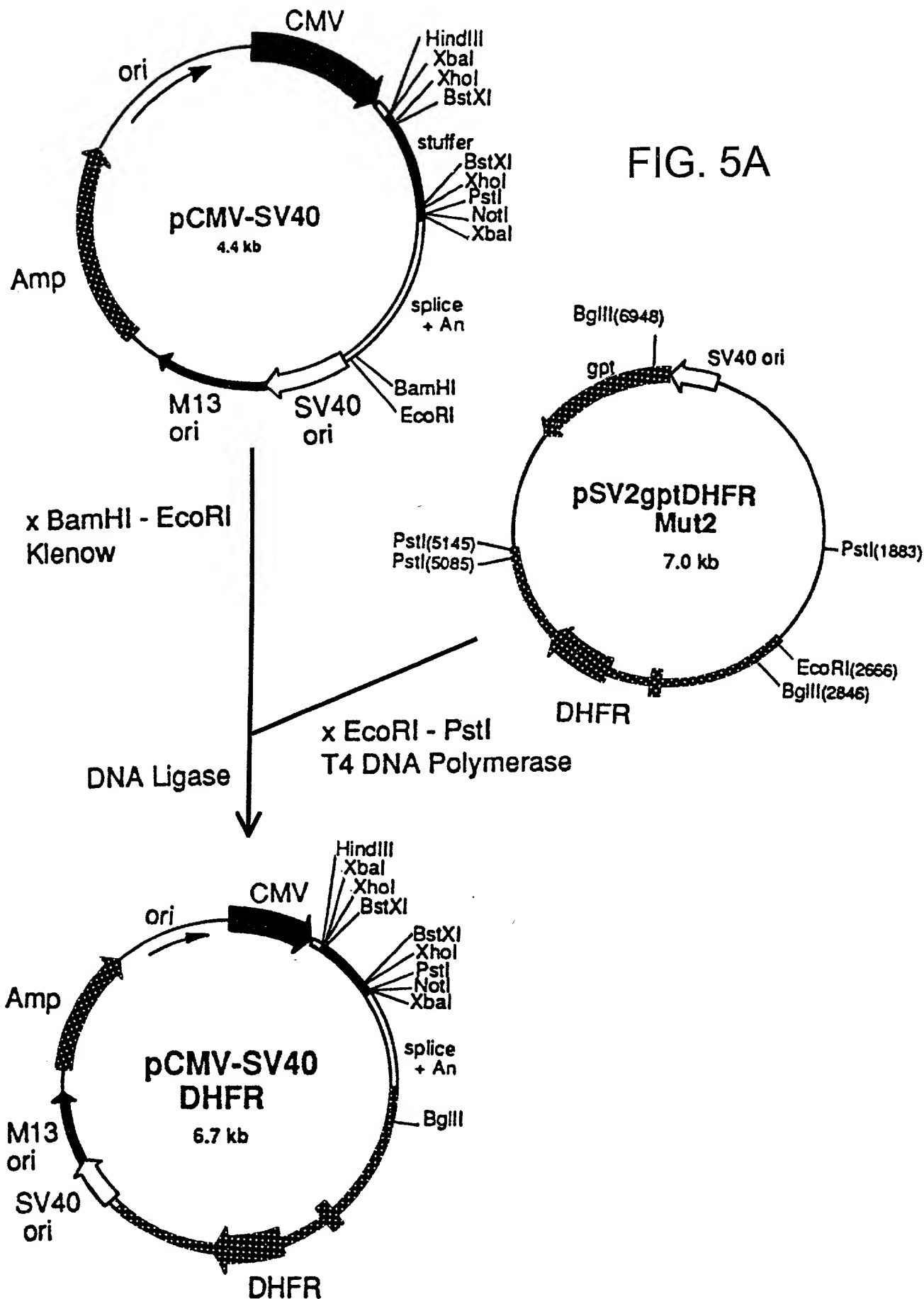


FIG. 5B

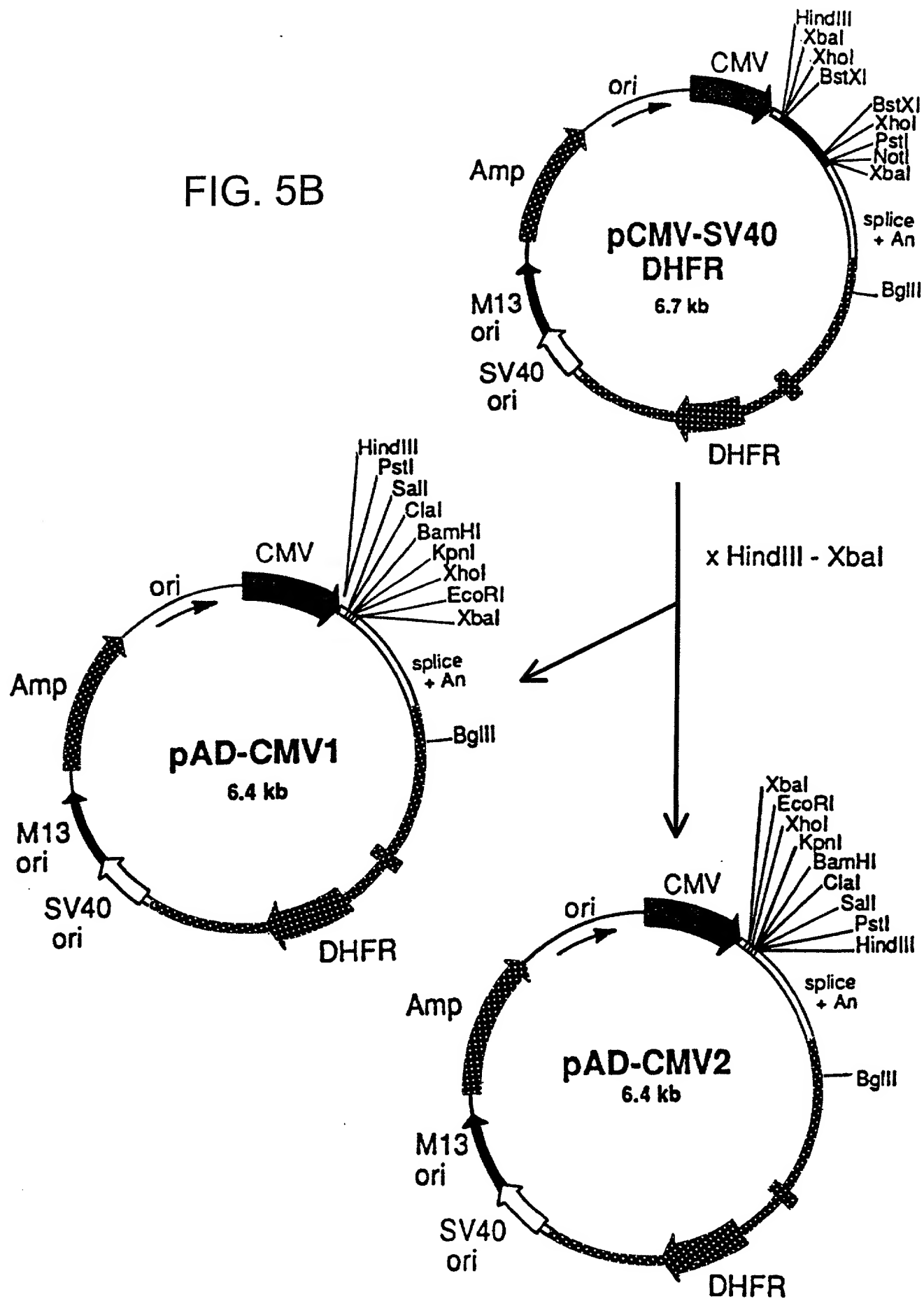


FIG. 5B

FIG. 6A

pAD-CMV1 : 6414 bp

TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAATT ACGGGGTCAT TAGTTCATAG	60
CCCATATATG GAGTTCCGCG TTACATAACT TACGGTAAAT GGCCCGCCTG GCTGACCGCC	120
CAACGACCCC CGCCCATTGA CGTCAATAAT GACGTATGTT CCCATAGTAA CGCCAATAGG	180
GACTTTCCAT TGACGTCAAT GGGTGGAGTA TTTACGGTAA ACTGCCCACT TGGCAGTACA	240
TCAAGTGTAT CATATGCCAA GTACGCCCCC TATTGACGTC AATGACGGTA AATGGCCCCG	300
CTGGCATTAT GCCCAGTACA TGACCTTATG GGACTTTCCT ACTTGGCAGT ACATCTACGT	360
ATTAGTCATC GCTATTACCA TGGTGATGCG GTTTTGGCAG TACATCAATG GCGTGGAATA	420
GCGGTTTGAC TCACGGGGAT TTCCAAGTCT CCACCCCAT TACGTCAATG GGAGTTTGTT	480
TTGGCACCAA AATCAACGGG ACTTTCCAAA ATGTCGTAAC AACTCCGCCC CATTGACGCA	540
AATGGGCGGT AGGCGTGTAC GGTGGGAGGT CTATATAAGC AGAGCTCTCT GGCTAACTAG	600
AGAACCCACT GCTTAACTGG CTTATCGAAA TTAATACGAC TCACTATAGG GAGACCCAAG	660
CTTCTGCAGG TCGACATCGA TGGATCCGGT ACCTCGAGCG CGAATTCTCT AGAGGATCTT	720
TGTGAAGGAA CCTTACTTCT GTGGTGTGAC ATAATTGGAC AAACCTACCTA CAGAGATTTA	780
AAGCTCTAAG GTAAATATAA AATTTTTAAG TGTATAATGT GTTAACTAC TGATTCTAAT	840
TGTTTGTGTA TTTTAGATTC CAACCTATGG AACTGATGAA TGGGAGCAGT GGTGGAATGC	900
CTTTAATGAG GAAAACCTGT TTTGCTCAGA AGAAATGCCA TCTAGTGATG ATGAGGCTAC	960
TGCTGACTCT CAACATTCTA CTCCTCCAAA AAAGAAGAGA AAGGTAGAAG ACCCCAAGGA	1020
CTTCCCTTCA GAATTGCTAA GTTTTTTGAG TCATGCTGTG TTTAGTAATA GAACTCTTGC	1080
TTGCTTTGCT ATTTACACCA CAAAGGAAAA AGCTGCACTG CTATACAAGA AAATTATGGA	1140
AAAATATTTG ATGTATAGTG CCTTGACTAG AGATCATAAT CAGCCATACC ACATTTGTAG	1200
AGGTTTTACT TGCTTTAAAA AACCTCCAC ACCTCCCCCT GAACCTGAAA CATAAAATGA	1260
ATGCAATTGT TGTGTGTAAC TTGTTTATTG CAGCTTATAA TGGTTACAAA TAAAGCAATA	1320
GCATCACAAA TTTCACAAAT AAAGCATTTT TTCACTGCA TTCTAGTTGT GGTTTGTCCA	1380
AACTCATCAA TGTATCTTAT CATGTCTGGA TCAATTCTGA GAACTAGCC TTAAAGACAG	1440

FIG. 6B

ACAGCTTTGT TCTAGTCAGC CAGGCAAGCA TATGTAAATA AAGTTCCTCA GGGAAC TGAG 1500

GTTAAAAGAT GTATCCTGGA CCTGCCAGAC CTGGCCATTC ACGTAAACAG AAGATTCCGC 1560

CTCAAGTTCC GGTTAACAAC AGGAGGCAAC GAGATCTCAA ATCTATTACT TCTAATCGGG 1620

TAATTAAAAC CTTTCAACTA AAACACGGAC CCACGGATGT CACCCACTTT TCCTTCCCCG 1680

GCTCCGCCCT TCTCAGTACT CCCACCAT T AGGCTCGCTA CTCCACCTCC ACTTCCGGGC 1740

GCGACACCCA CGTGCCCTCT CCCACCCGAC GCTAACCCCG CCCCTGCCCC TCTGACCCCG 1800

CCCACCACCT GGCCCCGCC CGTTGAGGAC AGAAGAAACC CCGGGCAGCC GCAGCCAAGG 1860

CGGACGGGTA GACGCTGGGG GCGCTGAGGA GTCGTCTCT ACCTTCTCTG CTGGCTCGGT 1920

GGGGGACGCG GTGGATCTCA GGCTTCCGGA AGACTGGAAG AACC GGCTCA GAACCGCTTG 1980

TCTCCGCGGG GCTTGGGCGG CGGAAGAATG GCCGCTAGAC GCGGACTTGG TGCGAGGCAT 2040

CGCAGGATGC AGAAGAGCAA GCGCGCCGGG AGCGCGCGGC TGTACTACCC CGCGCCTGGA 2100

GCGGCCACGC CGGACTGGGC GGGGCCGGCC TGGTGGAGGC GGAGTCTGAC CTCGTGGAGG 2160

CGGGGCCTCT GATGTTCAA TAGGATGCTA GGCTTGTTGA GCGTGGCCT CCGATTCACA 2220

AGTGGAAGC AGCGCCGGGC GACTGCAATT TCGCGCCAAA CTTGGGGGAA GCACAGCGTA 2280

CAGGCTGCCT AGGTGATCGC TGCTGCTGTC ATGGTTCGAC CGCTGAACTG CATCGTCGCC 2340

GTGTCCCAGA ATATGGGCAT CGGCAAGAAC GGAGACCTTC CCTGGCCAAT GCTCAGGTAC 2400

TGGCTGGATT GGGTTAGGGA AACC GAGGCG GTTCGCTGAA TCGGGTCGAG CACTTGGCGG 2460

AGACGCGCGG GCCAACTACT TAGGGACAGT CATGAGGGGT AGGCCCCGCC GCTGCTGCCC 2520

TTGCCCATGC CCGCGGTGAT CCCCATGCTG TGCCAGCCTT TGCCAGAGG CGCTCTAGCT 2580

GGGAGCAAAG TCCGGTCACT GGGCAGCACC ACCCCCCGGA CTTGCATGGG TAGCCGCTGA 2640

GATGGAGCCT GAGCACACGT GACAGGGTCC CTGTTAACGC AGTGTTTCTC TAACTTTCAG 2700

GAACGAGTTC AAGTACTTCC AAAGAATGAC CACCACCTCC TCAGTGGAAG GTAAACAGAA 2760

CCTGGTGATT ATGGGCCGGA AAACCTGGTT CTCCATTCTT GAGAAGAATC GACCTTTAAA 2820

GGACAGAATT AATATAGTTC TCAGTAGAGA GCTCAAGGAA CCACCACAAG GAGCTCATTT 2880

TCTTGCCAAA AGTCTGGACC ATGCCTTAAA ACTTATTGAA CAACCAGAGT TAGCAGATAA 2940

AGTGGACATG GTTTGGATAG TTGGAGGCAG TTCCGTTTAC AAGGAAGCCA TGAATCAGCC 3000

099429 6245660

FIG. 6C

AGGCCATCTC AGACTCTTTG TGACAAGGAT CATGCAGGAA TTTGAAAGTG ACACGTTCTT 3060
 CCCAGAAATT GATTGGAGA AATATAAACT TCTCCCAGAG TACCCAGGGG TCCTTTCTGA 3120
 AGTCCAGGAG GAAAAAGGCA TCAAGTATAA ATTTGAAGTC TATGAGAAGA AAGGCTAACA 3180
 GAAAGATACT TGCTGATTGA CTTCAAGTTC TACTGCTTTC CTCCTAAAAT TATGCATTTT 3240
 TACAAGACCA TGGGACTTGT GTTGGCTTTA GATCCTGTGC ATCCTGGGCA ACTGTTGTAC 3300
 TCTAAGCCAC TCCCCAAAGT CATGCCCCAG CCCCTGTATA ATTCTAAACA ATTAGAATTA 3360
 TTTTCATTTT CATTAGTCTA ACCAGGTTAT ATTAAATATA CTTTAAGAAA CACCATTGTC 3420
 CATAAAGTTC TCAATGCCCC TCCCATGCAG CCTCAAGTGG CTCCCCAGCA GATGCATAGG 3480
 GTAGTGTGTG TACAAGAGAC CCCAAAGACA TAGAGCCCCT GAGAGCATGA GCTGATATGG 3540
 GGGCTCATAG AGATAGGAGC TAGATGAATA AGTACAAAGG GCAGAAATGG GTTTTAACCA 3600
 GCAGAGCTAG AACTCAGACT TTAAAGAAAA TTAGATCAAA GTAGAGACTG AATTATTCTG 3660
 CACATCAGAC TCTGAGCAGA GTTCTGTTCA CTCAGACAGA AAATGGGTAA ATTGAGAGCT 3720
 GGCTCCATTG TGCTCCTTAG AGATGGGAGC AGGTGGAGGA TTATATAAGG TCTGGAACAT 3780
 TTAACCTCTC CGTTTCTCAT CTTCAAGTGG ATTCCAAGGG ATACTACAAT TCTGTGGAAT 3840
 GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG TATGCAAAGC 3900
 ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA 3960
 AGTATGCAAA GCATGCATCT CAATTAGTCA GCAACCATAG TCCCGCCCCT AACTCCGCCC 4020
 ATCCCGCCCC TAACTCCGCC CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT 4080
 TTTATTTATG CAGAGGCCGA GCGCCTCTG AGCTATTCCA GAAGTAGTGA GGAGGCTTTT 4140
 TTGGAGGCCT AGGCTTTTGC AAAAAAGCTA ATTCAGCCTG AATGGCGAAT GGGACGCGCC 4200
 CTGTAGCGGC GCATTAAGCG CGGCGGGTGT GGTGGTTACG CGCAGCGTGA CCGCTACACT 4260
 TGCCAGCGCC CTAGCGCCCG CTCCTTTTCGC TTTCTTCCCT TCCTTTCTCG CCACGTTTCGC 4320
 CGGCTTTCCC CGTCAAGCTC TAAATCGGGG GCTCCCTTTA GGGTTCCGAT TTAGTGCTTT 4380
 ACGGCACCTC GACCCCAAAA ACTTGATTAG GGTGATGGTT CACGTAGTGG GCCATCGCCC 4440
 TGATAGACGG TTTTTCGCCC TTTGACGTTG GAGTCCACGT TCTTTAATAG TGGACTCTTG 4500
 TTCCAAACTG GAACAACACT CAACCCTATC TCGGTCTATT CTTTGTATTT ATAAGGGATT 4560

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FIG. 6E

TCGGGCTGAA CGGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA 6180
CTGAGATACC TACAGCGTGA GCATTGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGGCG 6240
GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGA GCTTCCAGGG 6300
GGAAACGCCT GGTATCTTTA TAGTCCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA 6360
TTTTTGTGAT GCTCGTCAGG GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCC

FIG. 6E 6245550

0000420 6246860

FIG. 7A

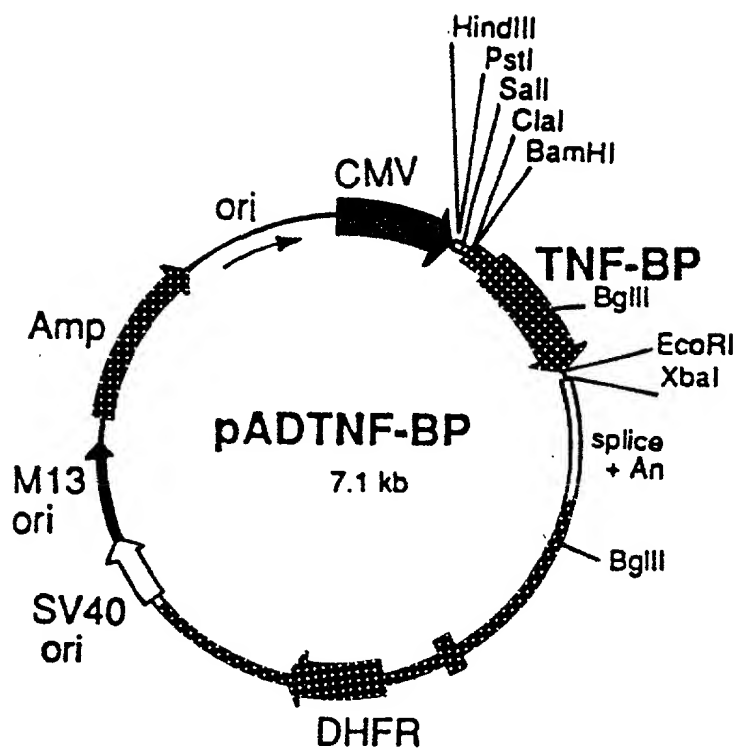


FIG. 7B

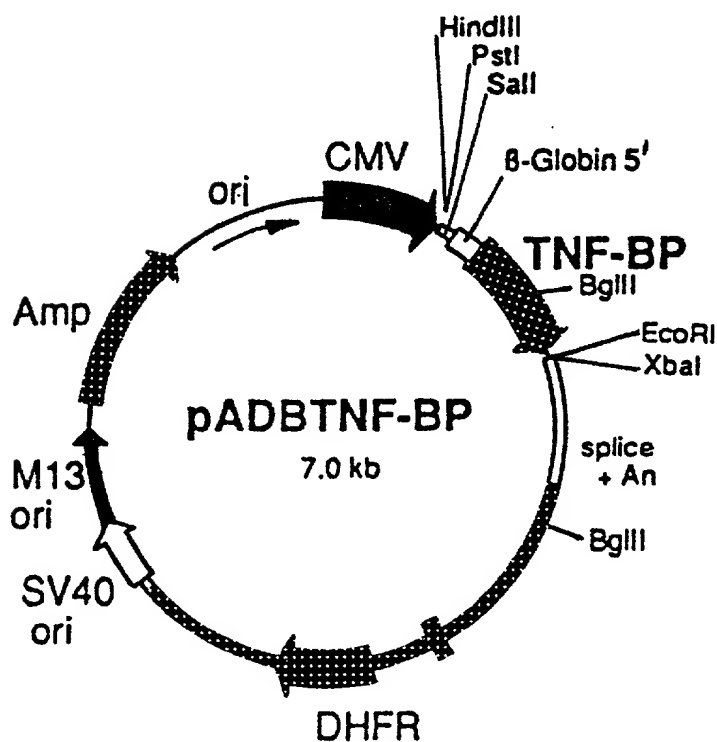


FIG. 7C

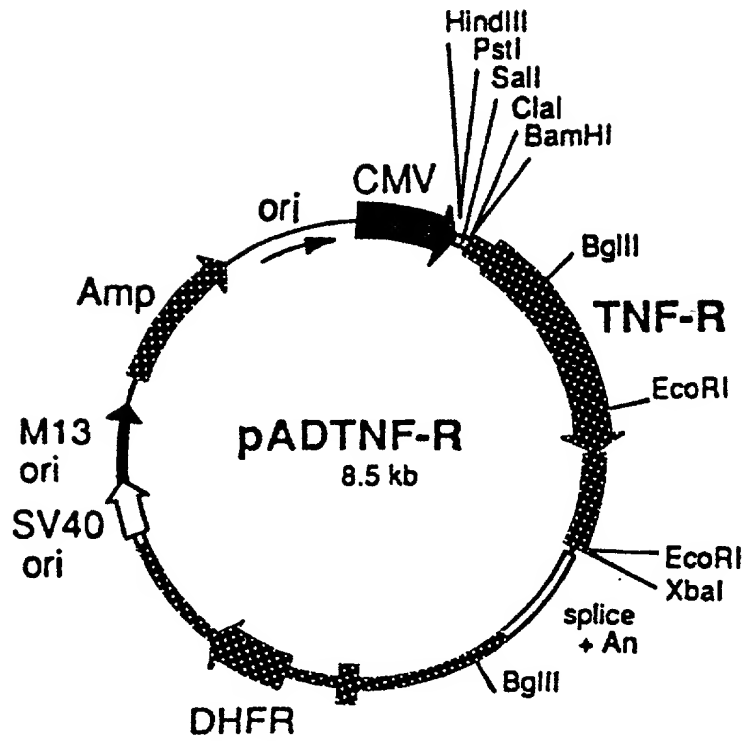


FIG. 7D

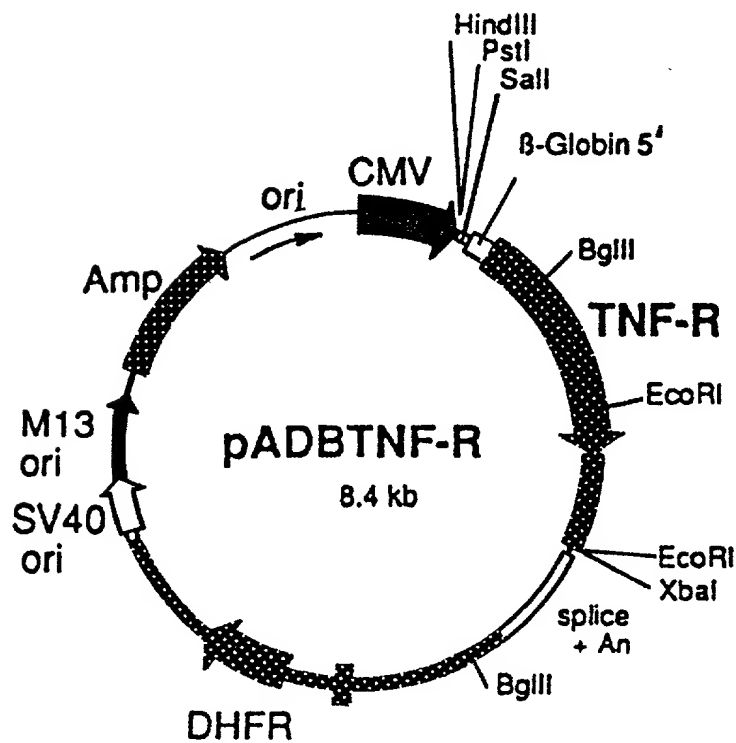


FIG. 8A

raTNF-R

GAATTCCTTT	TCTCCGAGTT	TTCTGAACTC	TGGCTCATGA	TCGGGCTTAC	TGGATACGAG	60
AATCCTGGAG	GACCGTACCC	TGATTTCAT	CTACCTCTGA	CTTTGAGCCT	TTCTAACCCG	120
GGGCTCACGC	TGCCAACACC	CGGGCCACCT	GGTCCGATCG	TCTTACTTCA	TTACCAGCG	180
TTGCCAATTG	CTGCCCTGTC	CCCAGCCCCA	ATGGGGGAGT	GAGAGAGGCC	ACTGCCGGCC	240

GGAC

245/1	275/11
ATG GGT CTC CCC ATC GTG CCT GGC CTG CTG CTG TCA CTG GTG CTC CTG GCT CTG CTG ATG	
Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu Leu Ala Leu Leu Met	
305/21	335/31
GGG ATA CAC CCA TCA GGG GTC ACC GGA CTG GTT CCT TCT CTT GGT GAC CGG GAG AAG AGG	
Gly Ile His Pro Ser Gly Val Thr Gly Leu Val Pro Ser Leu Gly Asp Arg Glu Lys Arg	
365/41	395/51
GAT AAT TTG TGT CCC CAG GGA AAG TAT GCC CAT CCA AAG AAT AAT TCC ATC TGC TGC ACC	
Asp Asn Leu Cys Pro Gln Gly Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr	
425/61	455/71
AAG TGC CAC AAA GGA ACC TAC TTG GTG AGT GAC TGT CCA AGC CCA GGG CAG GAA ACA GTC	
Lys Cys His Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr Val	
485/81	515/91
TGC GAG CTC TCT CAT AAA GGC ACC TTT ACA GCT TCG CAG AAC CAC GTC AGA CAG TGT CTC	
Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His Val Arg Gln Cys Leu	
545/101	575/111
AGT TGC AAG ACA TGT CGG AAA GAA ATG TTC CAG GTG GAG ATT TCT CCT TGC AAA GCT GAC	
Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln Val Glu Ile Ser Pro Cys Lys Ala Asp	
605/121	635/131
ATG GAC ACC GTG TGT GGC TGC AAG AAG AAC CAA TTC CAG CGC TAC CTG AGT GAG ACG CAT	
Met Asp Thr Val Cys Gly Cys Lys Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His	
665/141	695/151
TTC CAG TGT GTG GAC TGC AGC CCC TGC TTC AAT GGC ACC GTG ACA ATC CCC TGT AAG GAG	
Phe Gln Cys Val Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys Glu	
725/161	755/171
AAA CAG AAC ACC GTG TGT AAC TGC CAC GCA GGA TTC TTT CTA AGC GGA AAT GAG TGC ACC	
Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly Asn Glu Cys Thr	
785/181	815/191
CCT TGC AGC CAC TGC AAG AAA AAT CAG GAA TGT ATG AAG CTG TGC CTA CCT CCA GTT GCA	
Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys Met Lys Leu Cys Leu Pro Pro Val Ala	
845/201	875/211
AAT GTC ACA AAC CCC CAG GAC TCA GGT ACT GCC GTG CTG TTG CCT CTG GTT ATC TTC CTA	
Asn Val Thr Asn Pro Gln Asp Ser Gly Thr Ala Val Leu Leu Pro Leu Val Ile Phe Leu	
905/221	935/231
GGT CTT TGC CTT TTA TTC TTT ATC TGC ATC AGT CTA CTG TGC CGA TAT CCC CAG TGG AGG	
Gly Leu Cys Leu Leu Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg	
965/241	995/251
CCC AGG GTC TAC TCC ATC ATT TGT AGG GAT TCA GCT CCT GTC AAA GAG GTG GAG GGT GAA	
Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys Glu Val Glu Gly Glu	
1025/261	1055/271
GGA ATT GTT ACT AAG CCC CTA ACT CCA GCC TCT ATC CCA GCC TTC AGC CCC AAC CCC GGC	
Gly Ile Val Thr Lys Pro Leu Thr Pro Ala Ser Ile Pro Ala Phe Ser Pro Asn Pro Gly	
1085/281	1115/291
TTC AAC CCC ACT CTG GGC TTC AGC ACC ACC CCA CGC TTC AGT CAT CCT GTC TCC AGT ACC	
Phe Asn Pro Thr Leu Gly Phe Ser Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr	
1145/301	1175/311
CCC ATC AGC CCC GTC TTC GGT CCT AGT AAC TGG CAC AAC TTC GTG CCA CCT GTA AGA GAG	
Pro Ile Ser Pro Val Phe Gly Pro Ser Asn Trp His Asn Phe Val Pro Pro Val Arg Glu	
1205/321	1235/331
GTG GTC CCA ACC CAG GGT GCT GAC CCT CTC CTC TAC GGA TCC CTC AAC CCT GTG CCA ATC	
Val Val Pro Thr Gln Gly Ala Asp Pro Leu Leu Tyr Gly Ser Leu Asn Pro Val Pro Ile	

FIG. 8A

FIG. 8B

1265/341 1295/351
 CCC GCC CCT GTT CGG AAA TGG GAA GAC GTC GTC GCG GCC CAG CCA CAA CGG CTT GAC ACT
 Pro Ala Pro Val Arg Lys Trp Glu Asp Val Val Ala Ala Gln Pro Gln Arg Leu Asp Thr
 1325/361 1355/371
 GCA GAC CCT GCG ATG CTG TAT GCT GTG GTG GAT GGC GTG CCT CCG ACA CGC TGG AAG GAG
 Ala Asp Pro Ala Met Leu Tyr Ala Val Val Asp Gly Val Pro Pro Thr Arg Trp Lys Glu
 1385/381 1415/391
 TTC ATG CGG CTC CTG GGG CTG AGC GAG CAC GAG ATC GAG CGG CTG GAG CTG CAG AAC GGG
 Phe Met Arg Leu Leu Gly Leu Ser Glu His Glu Ile Glu Arg Leu Glu Leu Gln Asn Gly
 1445/401 1475/411
 CGT TGC CTC CGC GAG GCT CAT TAC AGC ATG CTG GAA GCC TGG CGG CGC CGC ACA CCG CGA
 Arg Cys Leu Arg Glu Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg Arg Thr Pro Arg
 1505/421 1535/431
 CAC GAG GCC ACG CTG GAC GTA GTG GGC CGC GTG CTT TGC GAC ATG AAC CTG CGT GGC TGC
 His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu Cys Asp Met Asn Leu Arg Gly Cys
 1565/441 1595/451
 CTG GAG AAC ATC CGC GAG ACT CTA GAA AGC CCT GCC CAC TCG TCC ACG ACC CAC CTC CCG
 Leu Glu Asn Ile Arg Glu Thr Leu Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro
 1625/461
 CGA TAA
 Arg Stop

GGCCACACCC CCACCTCAGG AACGGGACTC GAAGGACCAT CCTGCTAGAT 1680
 GCCCTGCTTC CCTGTGAACC TCCTCTTTGG TCCTCTAGGG GGCAGGCTCG ATCTGGCAGG 1740
 CTCGATCTGG CAGCCACTTC CTTGGTGCTA CCGACTTGGT GTACATAGCT TTTCCCAGCT 1800
 GCCGAGGACA GCCTGTGCCA GCCACTTGTG CATGGCAGGG AAGTGTGCCA TCTGCTCCCA 1860
 GACAGCTGAG GGTGCCAAAA GCCAGGAGAG GTGATTGTGG AGAAAAAGCA CAATCTATCT 1920
 GATACCCACT TGGGATGCAA GGACCCAAAC AAAGCTTCTC AGGGCCTCCT CAGTTGATTT 1980
 CTGGGCCCTT TTCACAGTAG ATAAACAGT CTTTGTATTG ATTATATCAC ACTAATGGAT 2040
 GAACGGTTGA ACTCCCTAAG GTAGGGGCAA GCACAGAACA GTGGGGTCTC CAGCTGGAGC 2100
 CCCC GACTCT TGTAATACA CTAAAAATCT AAAAGTGAAA AAAAAAAAAA AAAAAAAAAA 2160
 AAAAAAGGAA TTC

FIG. 8B

FIG. 9B

1233/341 1263/351
TGG GAG GAC AGC GCC CAC AAG CCA CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC
Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr
1293/361 1323/371
GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC TGG AAG GAA TTC GTG CGG CGC CTA GGG CTG
Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu
1353/381 1383/391
AGC GAC CAC GAG ATC GAT CGG CTG GAG CTG CAG AAC GGG CGC TGC CTG CGC GAG GCG CAA
Ser Asp His Glu Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
1413/401 1443/411
TAC AGC ATG CTG GCG ACC TGG AGG CGG CGC ACG CCG CGG CGC GAG GCC ACG CTG GAG CTG
Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu
1473/421 1503/431
CTG GGA CGC GTG CTC CGC GAC ATG GAC CTG CTG GGC TGC CTG GAG GAC ATC GAG GAG GCG
Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala
1533/441 1563/451
CTT TGC GGC CCC GCC GCC CTC CCG CCC GCG CCC AGT CTT CTC AGA TGA 1580
Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg Stop

GGCTGCGCCC CTGCGGGCAG CTCTAAGGAC CGTCCTGCGA 1620
GATCGCCTTC CAACCCCACT TTTTCTGGA AAGGAGGGGT CCTGCAGGGG CAAGCAGGAG 1680
CTAGCAGCCG CCTACTTGGT GCTAACCCT CGATGTACAT AGCTTTTCTC AGCTGCCTGC 1740
GCGCCGCCGA CAGTCAGCGC TGTGCGCGCG GAGAGAGGTG CGCCGTGGGC TCAAGAGCCT 1800
GAGTGGGTGG TTTGCGAGGA TGAGGGACGC TATGCCTCAT GCCCGTTTTG GGTGTCCTCA 1860
CCAGCAAGGC TGCTCGGGGG CCCCTGGTTC GTCCCTGAGC CTTTTTCACA GTGCATAAGC 1920
AGTTTTTTTT GTTTTTGTTT TGTTTTGTTT TGTTTTTAAA TCAATCATGT TACACTAATA 1980
GAACTTGGC ACTCCTGTGC CCTCTGCCTG GACAAGCACA TAGCAAGCTG AACTGTCCTA 2040
AGGCAGGGGC GAGCACGGAA CAATGGGGCC TTCAGCTGGA GCTGTGGACT TTTGTACATA 2100
CACTAAAATT CTGAAGTTAA AAAAAAAAAA AAAAGGAATT C 2141

FIG. 9B

FIG.10

